

13 cont.

ATSV	M472	CTGGATCCCCGGGGCTTCGGTGAAGGTGGCG (SEQ ID NO:86) CACTCGAGCATCTCGGCCAGCAGGGCTTC (SEQ ID NO:87)	G3-M472	5': BamHI 3': XhoI	pET23dmyc
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Please insert the accompanying paper copy of the sequence listing, pages 1-19, at the end of the end of the application.

REMARKS

Applicants request entry of this amendment in adherence with 37 C.F.R. §§ 1.821-1.825. This amendment is accompanied by a computer disk containing the above named sequences, SEQ ID NO:1-87, in computer readable form, and a paper copy of the sequence information that has been prepared from the computer disk.

The information contained in the computer disk was prepared using the software program "PatentIn" and is identical to the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made in the specification by the amendment. The attached pages are entitled "VERSION WITH MARKINGS TO SHOW CHANGES MADE".

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

Please amend Table 1, beginning on page 34, line 22, as follows:

Table 1: Cloning of Human kinesins

Human kinesin	Published Seq: Accession #s & Publication Ref.	Primers for cDNA cloning: 5' primer (SEQ ID NO:) 3' primer (SEQ ID NO:)	Nucleotides Included	cDNA Source
Chromo-kinesin	AF071592 1165722(GSDB – partial)	RACE AP1 primer (Clontech) CCAAACAGGAAACAGTATCCAAGGCAACC (SEQ ID NO:1)	<1-193	Marathon-Ready HeLa (Clontech)
		TGCCCATCTCGTGAGAAAGC (SEQ ID NO:2) GCTTGACGGAGAGCATGCTG (SEQ ID NO:3)	76-1178	HeLa (Our prep)
		ATTGATTACCCAGTTATCGG (SEQ ID NO:4) TGATGACTCCAACCTTCAGTG (SEQ ID NO:5)	1032-3326	HeLa (Our prep)
Kin-2	Y08319	GCCGAATACATCAAGCAATGGTAAC (SEQ ID NO:6) TCTGGGTATCCTTTAGCAGCAAATG (SEQ ID NO:7)	2-2088	Breast tumor (Invitrogen)
MKLP1	X67155 Nislow, et al. 1992	AGCCATGTTGTCAGCGAGAGCTAAG (SEQ ID NO:8) AGGGTCTCTCTGGCTTCTCAGTTTTAGG (SEQ ID NO:9)	73-2078	human placenta (Invitrogen)
KSP	U37426	CCTTGATTTTTTGGCGGGGACCGTC (SEQ ID NO:10) AAAGGTTGATCTGGGCTCGCAGAGG (SEQ ID NO:11)	66-3259	breast tumor (Invitrogen)
CENP-E	Z15005 Yen, et al. 1992			
MCAK	U63743 Kim, et al. 1997	GCGTTTCTCTTCCTTGCTGACTCTC (SEQ ID NO:12) AGAGGCTGGGTGTCAAACCAAACAG (SEQ ID NO:13)	22-2274	breast tumor (Invitrogen)

Kid	AB017430	GTCGCTGTCGGCTAAGCAAG (SEQ ID NO:14) CTTTGCCCCTGTGACTGTGC (SEQ ID NO:15)	101-1596	breast tumor (Invitrogen)
		CTGGATCCCAGCCGCGGGCGGCTCGACG CAG (SEQ ID NO:16) CTCTAGAGAGCAGCTGTCCATGCCCC (SEQ ID NO:17)	28-248	HeLa (our prep)
HSET	D14678 (partial)	GGGCTTGGTGCAAGAGCTTC (SEQ ID NO:18) CACCCCTCACCCGATACATAGAC (SEQ ID NO:19)	213-1624	HeLa (our prep)
ATSV	X90840	GGGCTCCCACTACTGCGAGG (SEQ ID NO:20) CTCCTCCTCGTTCACCTCCG (SEQ ID NO:21)	21-2311	WERI (our prep)

Please amend the paragraph beginning on page 35, line 18, as follows:

pET23d (Novagen 69748-3) encodes a T7 epitope tag 5' of the polylinker cloning site and a 6-His tag 3' of the polylinker cloning site. We constructed pET23dmyc by inserting the annealed oligonucleotides described below into the XhoI site of pET23d. This creates coding sequence for the myc epitope tag in-frame with the 6-His tag.

Annealed oligonucleotides for pET23dmyc:

sense: TCGAGGGTACCGAGCAGAAGCTGATCAGCGAGGAGGACCTGA
(SEQ ID NO:22)

antisense: TCGATCAGGTCCTCCTCGCTGATCAGCTTCTGCTCGGTACCC
(SEQ ID NO:23)

Please amend Table 2 beginning on page 37 as follows:

Table II: Subcloning of Human kinesins into Bacterial Expression Plasmids:

Kinesin	Construct Name	5' primer (SEQ ID NO) 3' primer (SEQ ID NO)	Residues Included	Cloning sites	Host Vector
Chromo-kinesin	K335	TAGCCATGGAAGAGGTGAAGGGAATTC (SEQ ID NO:24) CCGCTCGAGTTTCTTGCTCTGTC (SEQ ID NO:25)	E2-K335	5': NcoI 3': XhoI	pET23dmyc

Chromo- kinesin	Q475	TAGAAGCTTGGAAGAGGTGAAGGG (SEQ ID NO:26) TAGAAGCTTCTGGGTAATCAATTG (SEQ ID NO:27)	E2- Q475	5' Hind III 3': HindIII	pET23dmyc
Chromo- kinesin	D679	TAGAAGCTTGGAAGAGGTGAAGGG (SEQ ID NO:28) TAGAAGCTTGTCTCGTTCTTTAAC (SEQ ID NO:29)	E2- D679	5' Hind III 3': HindIII	pET23dmyc
Chromo- kinesin	FL1	TAGAAGCTTGGAAGAGGTGAAGGG (SEQ ID NO:30) TAGAAGCTTGTGGGCCTCTTCTCG (SEQ ID NO:31)	E2- H1229	5' Hind III 3': HindIII	pET23dmyc
Kin2	P166	TACGGATCCCAAATTATGAAATTATG (SEQ ID NO:32) TACAAGCTTAGCAGTTGGATCTACAGTC (SEQ ID NO:33)	P166- A532	5': BamHI 3': HindIII	pET23dmyc
Kin2	H195	TACGGATCCATAGGATATGTGTGTGTG (SEQ ID NO:34) TACAAGCTTAGCAGTTGGATCTACAGTC (SEQ ID NO:35)	H195- A532	5': BamHI 3': HindIII	pET23dmyc
Kin2	FL2	CTCCATGGTAACATCTTTAAATGAAGATAATG (SEQ ID NO:36) CTAAGCTTAAGGGCACGGGGTCTCTTCGGGTTG (SEQ ID NO:37)	M1- L679	5': NcoI 3': HindIII	pET23dmyc
MKLP1	E433	ATCCATGGCGAGAGCTAAGACACCCCGGAAACC (SEQ ID NO:38) ATGCGGCCGCTTCTTGAGTCACTTCCGCAAATCT C (SEQ ID NO:39)	A4- E433	5': NcoI 3': NotI	pET23dmyc
MKLP1	R494	ATCCATGGCGAGAGCTAAGACACCCCGGAAACC (SEQ ID NO:40) ATGCGGCCGCCCTTGGAAGTGTCTGCTCATCGTT G (SEQ ID NO:41)	A4- R494	5': NcoI 3': NotI	pET23dmyc
MKLP1	E658	ATCCATGGCGAGAGCTAAGACACCCCGGAAACC (SEQ ID NO:42) ATGCGGCCGCTTCAGTAACAATAGCCTTCAGTTG (SEQ ID NO:43)	A4- E658	5': NcoI 3': NotI	pET23dmyc
KSP	L360	ATCCATGGCGTGCCAGCCAAATTCGTCTGCG (SEQ ID NO:44) ATCTCGAGCAATATGTTCTTTGCTCTATGAGC (SEQ ID NO:45)	M1- L360	5': NcoI 3': XhoI	pET23dmyc
KSP	K491	ATCCATGGCGTGCCAGCCAAATTCGTCTGCG (SEQ ID NO:46) ATCTCGAGTTTCTCCTCAGTACTTTCCAAAGC (SEQ ID NO:47)	M1- K491	5': NcoI 3': XhoI	pET23dmyc
KSP	S553	ATCCATGGCGTGCCAGCCAAATTCGTCTGCG (SEQ ID NO:48) ATCTCGAGGCTGCCATCCTTAATTAATTCTTCC (SEQ ID NO:49)	M1- S553	5': NcoI 3': XhoI	pET23dmyc
CENP-E	M329	CTGGATCCCGGCGGAGGAAGGAGCCGTGGCC (SEQ ID NO:50) CACTCGAGCATATATTTAGCAGTACTGGC (SEQ ID NO:51)	A2- M329	5': BamHI 3': XhoI	pET23d

CENP-E	T340	CTGGATCCCGGCGGAGGAAGGAGCCGTGGCC (SEQ ID NO:52) CACTCGAGAGTTGATACCTCATTAACATAAGGAG (SEQ ID NO:53)	A2- T340	5': BamHI 3': XhoI	pET23d
CENP-E	S405	CTGGATCCCGGCGGAGGAAGGAGCCGTGGCC (SEQ ID NO:54) CACTCGAGAGAAGAGGTCACCAGCATCCG (SEQ ID NO:55)	A2- S405	5': BamHI 3': XhoI	pET23d
CENP-E	V465	CTGGATCCCGGCGGAGGAAGGAGCCGTGGCC (SEQ ID NO:56) CACTCGAGGACAGATTCATCAATTTCTCG (SEQ ID NO:57)	A2- V465	5': BamHI 3': XhoI	pET23d
CENP-E	T488	CTGGATCCCGGCGGAGGAAGGAGCCGTGGCC (SEQ ID NO:58) CACTCGAGTGTTGCTGGATTCCATTCTATC (SEQ ID NO:59)	A2- T488	5': BamHI 3': XhoI	pET23d
MCAK	M1	CTGGATCCGGAGGAAATCATGTCTTGTAAG (SEQ ID NO:60) CACTCGAGTGGAATCAGCGCCCCGTTAGAG (SEQ ID NO:61)	R189- P617	5': BamHI 3': XhoI	pET23dmyc
MCAK	M2	CTGGATCCCAAAGTGGGAATTTGCCGAATG (SEQ ID NO:62) CACTCGAGTGGAATCAGCGCCCCGTTAGAG (SEQ ID NO:63)	P228- P617	5': BamHI 3': XhoI	pET23dmyc
MCAK	M3	CTGGATCCACAGAATATGTGTCTGTGTTAGG (SEQ ID NO:64) CACTCGAGTGGAATCAGCGCCCCGTTAGAG (SEQ ID NO:65)	H257- P617	5': BamHI 3': XhoI	pET23dmyc
MCAK	M4	CTGGATCCGGAGGAAATCATGTCTTGTAAG (SEQ ID NO:66) CACTCGAGTGGTCCTTGCTGTATGATCTC (SEQ ID NO:67)	R189- P660	5': BamHI 3': XhoI	pET23dmyc
MCAK	M5	CTGGATCCCAAAGTGGGAATTTGCCGAATG (SEQ ID NO:68) CACTCGAGTGGTCCTTGCTGTATGATCTC (SEQ ID NO:69)	P228- P660	5': BamHI 3': XhoI	pET23dmyc
MCAK	M6	CTGGATCCACAGAATATGTGTCTGTGTTAGG (SEQ ID NO:70) CACTCGAGTGGTCCTTGCTGTATGATCTC (SEQ ID NO:71)	H257- P660	5': BamHI 3': XhoI	pET23dmyc
MCAK	FL3	CTCCATGGACTCGTCGCTTCAGGCCCGC (SEQ ID NO:72) CTCTCGAGCTGGGGCCGTTTCTTGCTGCTTATTT G (SEQ ID NO:73)	M3- Q725	5': NcoI 3': XhoI	pET23dmyc
Kid	A2N370	CTGGATCCCAGCCGCGGGCGGCTCGACGCAG (SEQ ID NO:74) CACTCGAGATTGATCACCTCCTTGACCTG (SEQ ID NO:75)	A2- N370	5': BamHI 3': XhoI	pET23dmyc
Kid	A2M511	CTGGATCCCAGCCGCGGGCGGCTCGACGCAG (SEQ ID NO:76) CACTCGAGCATTGTGGGACAATGGTTCTC (SEQ ID NO:77)	A2- M511	5': BamHI 3': XhoI	pET23dmyc

HSET	K519	TCGGATCCTTGGTGCAAGAGCTTCAG (SEQ ID NO:78) CACTCGAGCTTCCTGTTGGCCTGAGC (SEQ ID NO:79)	L72- K519	5': BamHI 3' XhoI	pET23dmyc
HSET	E152.2	CATGCCATGGAACCAAGGGCAAC (SEQ ID NO:80) CACTCGAGCTTCCTGTTGGCCTGAGC (SEQ ID NO:81)	E152- K519	5': NcoI 3': XhoI	pET23d
HSET	Q151.3	GGATATCCATATGCAGGAACCAAGGGCAAC (SEQ ID NO:82) GCAGGATCCTCACTTCCTGTTGGCCTGAG (SEQ ID NO:83)	Q151- K519	5': NdeI 3': BamHI	pET15b
ATSV	Q353	CTGGATCCCCGGGGCTTCGGTGAAGGTGGCG (SEQ ID NO:84) CACTCGAGCTGCTTGGCCCGGTCAGCATAC (SEQ ID NO:85)	G3-Q353	5': BamHI 3': XhoI	pET23dmyc
ATSV	M472	CTGGATCCCCGGGGCTTCGGTGAAGGTGGCG (SEQ ID NO:86) CACTCGAGCATCTCGGCCAGCAGGGCTTC (SEQ ID NO:87)	G3-M472	5': BamHI 3': XhoI	pET23dmyc